

GenCore version 5.1.6
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Om protein - protein search, using sw model
Run on: May 9, 2005, 20:59:41 ; Search time 39 Seconds
(without alignments)
44.408 Million cell updates/sec

Title: US-10-706-265-2
Perfect score: 121

Sequence: 1 RRWCYRKCYKGYCYRKCR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	106	87.6	18	2	JU0125	polyphemusin II -
2	103	85.1	18	2	JU0124	polyphemusin I - A
3	94	77.7	2	2	B38345	tachypleisin II pre-
4	91	75.2	17	2	JX0125	tachypleisin III -
5	88	72.7	17	2	A38824	tachypleisin I - ho
6	88	72.7	19	2	JX0124	tachypleisin I pre-
7	88	72.7	77	2	A38345	tachypleisin II pre-
8	82	43.0	594	2	T48087	transport inhibito
9	51	42.1	64	2	S32789	toxin II-14 - scor
10	50	41.3	85	2	C84867	probable trypsin i
11	50	41.3	922	2	T37256	metalloproteinase
12	48.5	40.1	970	2	T28234	ORF MSV076 probabili
13	48.5	39.7	86	2	JN0671	Na+-channel-blocker
14	48	39.7	90	2	B84867	probable trypain i
15	48	39.7	1184	2	D86387	probable protein P
16	47	38.8	345	2	T15599	hypothetical prote
17	47	38.8	1620	2	T27283	hypothetical prote
18	46.5	38.4	83	2	T03673	pitl protein (clon)
19	46.5	38.4	139	2	T18701	hypothetical prote
20	46.5	38.4	622	2	T37257	hypothetical prote
21	46	38.0	30	2	B60791	toxin II-6 - scor
22	46	38.0	376	2	B84867	hypothetical prote
23	46	38.0	650	2	T0094	endostyle-specific
24	46	38.0	749	2	T29859	mechanosensory pro
25	46	38.0	795	2	T20609	hypotheical prote
26	46	38.0	1390	2	T30346	insulin receptor
27	45.5	37.6	143	2	T24261	hypothetical prote
28	45	37.2	66	2	A31188	neurotoxin 1 - sco
29	45	37.2	68	2	AC1282	hypothetical prote

ALIGNMENTS

30	45	37.2	135	2	G84469	probable glycine-rich protein
31	45	37.2	251	2	A55035	cysteine-rich protein
32	45	37.2	361	1	F63555	conserved hypothetical protein
33	45	37.2	374	2	D81715	probable Ni/Fe-hyd
34	45	37.2	497	2	G81884	hypothetical protein
35	45	37.2	1148	2	A7446	hypothetical protein
36	44.5	36.8	144	2	T29558	hypothetical protein
37	44	36.4	131	2	T11557	hypothetical protein - similar
38	44	36.4	132	2	T11564	hypothetical protein
39	44	36.4	392	2	T32111	hypothetical protein
40	44	36.4	598	2	T40676	hypothetical protein
41	42	36.4	1251	2	A57293	latent transformin MEG6 protein - rarer
42	42	36.4	1574	2	T13554	hyperplastic discs
43	43	36.4	2895	2	T08437	similar to gibbere
44	43	36.4	108	2	G84322	hypothetical protein
45	43.5	36.0	217	2	T28343	

probable glycine-rich protein
cysteine-rich protein
conserved hypothetical protein
probable Ni/Fe-hyd

hypothetical protein
hypothetical protein - similar
hypothetical protein
hypothetical protein
hypothetical protein
latent transformin MEG6 protein - rarer
hyperplastic discs
similar to gibbere
hypothetical protein

A;Reference number:	A30069;	MUID:	89034158;	PMID:	3141410	
A;Accession:	A30069					
A;Molecule type:	protein					
A;Residues:	24-40 <NAK>					
Query Match	72.7%	Score	88;	DB	2;	
Best Local Similarity	64.7%	Pred.	No.	0	0.0017;	
Matches	11;	Conservative	4;	Mismatches	2;	
Indels	0;	Gaps	0;			
RESULT 8						
Qy	2 RWCYCKYCKYCKYCYRKCR 18					
Db	: : : : : 40					
Transport inhibitor response protein TIR1 [imported] - <i>Arabidopsis thaliana</i>						
transport inhibitor response protein TIR1 [imported] - <i>Arabidopsis thaliana</i> (mouse-ear cress)						
N;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)						
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004						
C;Accession: T48087; T51946						
R;Obermaier, B.; Otenwalder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem						
submitted to the Protein Sequence Database, April 2000						
A;Reference number: Z22484						
A;Accession: T48087						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-594 <OBE>						
A;Cross-references: UNIPROT:024660; EMBL:AL163816						
A;Experimental source: Cultivar Columbia; BAC clone T20010						
R;Ruegger, M.; Dewey, B.; Hobble, L.; Turner, J.; Estelle, M.						
submitted to the EMBL Data Library, May 1997						
A;Description: The TIR1 protein of <i>Arabidopsis</i> functions in auxin response and is relate						
A;Reference number: Z22581						
A;Status: preliminary; translated from GB/EMBL/DDBJ						
A;Residues: 1-594 <RUE>						
A;Cross-references: EMBL:AF005047; PIDN:AAB69175.1						
C;Genetics:						
A;Gene: TIR1						
A;Map position: 3						
A;Intron: 156/2; 320/3						
A;Note: T20010.80						
RESULT 9						
Query Match	43.0%	Score	52;	DB	2;	
Best Local Similarity	61.5%	Pred.	No.	21;	Length	594;
Matches	8;	Conservative	1;	Mismatches	4;	
Qy	2 RWCYCKYCKYCKYCY 14			Indels	0;	
Db	: : : : 54			Gaps	0;	
Scorpion (Centruroides noxius) toxin II-14						
Scorpion (Centruroides noxius)						
C;Species: Centruroides noxius						
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004						
C;Accession: S32789						
R;Possani, L.D.; Martin, B.M.; Svendsen, I.; Rode, G.S.; Erickson, B.W.						
Biochem. J. 229, 739-750, 1985						
A;Title: Scorpion toxins from <i>Centruroides noxius</i> and <i>Tityus serrulatus</i> . Primary structure						
A;Accession: S32789						
A;Status: preliminary						
A;Molecule type: protein						
A;Residues: 1-64 <POS>						
A;Cross-references: UNIPROT:PI5223						
C;Superfamily: scorpion neurotoxin						
Query Match	42.1%	Score	51;	DB	2;	
Best Local Similarity	47.4%	Pred.	No.	63;	Length	64;
Matches	9;	Conservative	2;	Mismatches	4;	
Indels	4;	Gaps	1;			
RESULT 10						
Query Match	41.3%	Score	50;	DB	2;	
Best Local Similarity	75.0%	Pred.	No.	49;	Length	922;
Matches	9;	Conservative	1;	Mismatches	0;	
Indels	2;	Gaps	1;			
Qy	9 YKGYC-YRKCR 18					
Db	: : : 29					
probable trypsin inhibitor [imported] - <i>Arabidopsis thaliana</i>						
C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)						
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004						
C;Accession: C84867						
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;						
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shan, M.; Vanaken, S.E.; Umayam, L.; Talon, L.						
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Venter, J.						
Nature 402, 761-768, 1999 analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> .						
A;Title: Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> .						
A;Reference number: A84420; MUID:2008487; PMID:10617197						
A;Accession: C84867						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-85 <STO>						
A;Cross-references: UNIPROT:022867; GB:AE002093; NID:92289007; PIDN:AAB64336.1; GSPDB:GN						
C;Genetics:						
A;Gene: At2g43530						
A;Map position: 2						
Query Match	41.3%	Score	50;	DB	2;	
Best Local Similarity	43.8%	Pred.	No.	10;	Length	85;
Matches	7;	Conservative	2;	Mismatches	7;	
Indels	0;	Gaps	0;			
Qy	3 WCYRKYCKYCYRKCR 18					
Db	: : : : 60					
metalloprotease sup-17 - <i>Caenorhabditis elegans</i>						
N;Species: ADAM 10 protein						
C;Species: <i>Caenorhabditis elegans</i>						
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004						
C;Accession: T37256; T20395						
R;Wen, C.; Mezzalira, M.M.; Greenwald, I.						
Development 124, 4759-4767, 1997						
A;Title: SUP-17, a <i>Caenorhabditis elegans</i> ADAM protein related to <i>Drosophila</i> KUZBANIAN,						
A;Reference number: 221649; MUID:98088688; PMID:9428412						
A;Accession: T37256						
A;Status: preliminary; translated from GB/EMBL/DDBJ						
A;Molecule type: mRNA						
A;Residues: 1-922 <WEN>						
A;Cross-references: UNIPROT:046354; EMBL:AF024614; NID:92739036; PIDN:AAB97161.1; PID:92						
R;Lennard, N.						
submitted to the EMBL Data Library, June 1997						
A;Reference number: Z19266						
A;Accession: T20395						
A;Status: preliminary; translated from GB/EMBL/DDBJ						
A;Molecule type: DNA						
A;Residues: 1-922 <WIL>						
A;Cross-references: EMBL:Z96047; PIDN:CA0916.1; GSPDB:GN00019; CESP:sup-17						
A;Experimental source: clone DY3						
A;Genetics:						
A;Gene: sup-17						
A;Map position: 1						
A;Introns: 47/3; 75/2; 117/1; 137/3; 181/2; 308/3; 331/3; 377/1; 441/1; 590/3; 664/1; 74						
Query Match	41.3%	Score	50;	DB	2;	
Best Local Similarity	75.0%	Pred.	No.	49;	Length	922;
Matches	9;	Conservative	1;	Mismatches	0;	
Indels	2;	Gaps	1;			
Qy	9 YKGYC-YRKCR 18					

RESULT 12

Db 703 YKGYCDIFRKCR 714
 A;Molecule type: DNA
 A;Residues: 1-90 <STO>
 A;Cross-references: UNIPROT:O22866; GB:AB002093; NID:92288995; PIDN:AAB64324.1; GSPDB:GNK
 C;Species: *Melanoplus sanguinipes* entomopoxvirus
 C;Accession: T28334 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
 J. Virol. 73, 533-552, 1999
 A;Title: The genome of *Melanoplus sanguinipes* entomopoxvirus.
 A;Reference number: ZZ0484; MUID:99102612; PMID:9847359
 A;Accession: T28334
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-970 <AF0>
 A;Cross-references: UNIPROT:Q9YW19; EMBL:AF063866; NID:94049647; PIDN: AAC97813.1; PID:94
 C;Note: MSV076

Query Match 40.1%; Score 48.5; DB 2; Length 970;
Best Local Similarity 52.9%; Pred. No. 79; 1; Mismatches 6; Indels 1; Gaps 1;
Matches 9; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 3 WCYRKCYKG-YCYRKCR 18
 Db 847 WPNRCPKGCVPCR 863

RESULT 13

JN0671 Na+-channel-blocking toxin (clone cngtIV) precursor - scorpion (*Centruroides noxius*)
 C;Species: *Centruroides noxius*
 C;Accession: JN0671 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Authors: Garcia, C.; Corona, M.; Bolivar, F.; Possani, L.D.
 Gene 128, 165-171, 1993
 R;Becerril, B.; Vazquez, A.; Garcia, C.; Corona, M.; Bolivar, F.; Possani, L.D.
 Gene 128, 165-171, 1993
 A;Title: Cloning and characterization of cDNAs that code for Na+-channel-blocking toxins
 A;Reference number: JN0669; MUID:93202983; PMID:8390386
 A;Accession: JN0671
 A;Molecule type: mRNA
 A;Residues: 1-86 <BEC>
 A;Cross-references: UNIPROT:P45665; GB:L05062; NID:9304570; PIDN:AAA28287.1; PID:9304571
 A;Experimental source: venom gland
 C;Superfamily: scorpion neurotoxin
 C;Keywords: toxin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-85/Product: Na+-channel-blocking toxin (clone cngtIV) #status predicted <MAT>

Query Match 39.7%; Score 48; DB 2; Length 86;
Best Local Similarity 42.1%; Pred. No. 18; 8; Mismatches 3; Indels 4; Gaps 1;
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

Qy 4 CYRKCYK---GYCYRKCR 18
 Db 30 CKNQYKLGENYCNECK 48

RESULT 14

B84867 probable trypsin inhibitor [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: B84867 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Authors: Rilliu, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Elsiss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Viral. 73, 533-552, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: B84867
 A;Status: preliminary

Query Match 39.7%; Score 48; DB 2; Length 90;
Best Local Similarity 37.5%; Pred. No. 19; 3; Mismatches 4; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 WCYRKCYKG-CY 14
 Db 915 WCYRKCYKG-CY 926

Search completed: May 9, 2005, 21:15:12
 Job time : 41 secs

RN [1]
 RP SSEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=90110066; PubMed=2514185;
 RA Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M.,
 RA Takao T., Shimomishi Y.;
 RT "Antimicrobial peptides, isolated from horseshoe crab hemocytes, and
 biological activity.";
 RL J. Biochem. 106:63-68(1989).
 CC -!- FUNCTION: Significantly inhibits the growth of Gram-negative and
 CC Gram-positive bacteria.
 CC -!- TISSUE SPECIFICITY: Hemocytes.
 CC -!- SIMILARITY: Belongs to the tachypleasin/polyphemusin family.
 DR PIR: B39345; B39345.
 DR HSSP; P4213; IMA2.
 KW Amidation; Antibiotic; Cleavage on pair of basic residues;
 KW Direct protein sequencing; Signal.
 FT SIGNAL 1
 FT PEPTIDE 24 40 23
 FT PROPEP 41 77
 FT DISULFID 26 39
 FT DISULFID 30 35
 FT MOD_RES 40 40
 FT DOMAIN 69 77
 SQ SEQUENCE 77 AA; 9335 MW; 6EBB57AA652ABFF CRC64;
 Query Match 77.7%; Score 94; DB 1; Length 77;
 Best Local Similarity 76.5%; Pred. No. 6e-05; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 13; Conservative 24 RWCFRVCYRGICYRKCR 40
 Db
 QY 2 RWCFRVCYRGICYRKCR 18
 DR PIR: JU0124; JU0124.
 DR HSSP; P14213; IMA2.
 KW Amidation; Antibiotic; Direct protein sequencing.
 FT DISULFID 4 17
 FT MOD_RES 8 13
 FT SEQUENCE 18 AA; 2459 MW; FB3FA109D2923504 CRC64;
 SQ SEQUENCE 77 AA; 9335 MW; 6EBB57AA652ABFF CRC64;
 Query Match 77.7%; Score 94; DB 1; Length 77;
 Best Local Similarity 76.5%; Pred. No. 6e-05; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 13; Conservative 24 RWCFRVCYRGICYRKCR 40
 DR PIR: JX0125; JX0125.
 DR HSSP; P4213; IMA2.
 KW Amidation; Antibiotic; Direct protein sequencing.
 KW Disulfide bond formation.
 CC -!- FUNCTION: Significantly inhibits the growth of Gram-negative and
 CC Gram-positive bacteria.
 CC -!- TISSUE SPECIFICITY: Hemocytes.
 CC -!- SIMILARITY: Belongs to the tachypleasin/polyphemusin family.
 DR PIR: JX0125; JX0125.
 DR HSSP; P4213; IMA2.
 KW Amidation; Antibiotic; Direct protein sequencing.
 FT DISULFID 3 16
 FT DISULFID 7 12
 FT MOD_RES 17 17
 SQ SEQUENCE 17 AA; 2241 MW; E9E08CE9D2923C94 CRC64;
 Query Match 75.2%; Score 91; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 3.9e-05; 3; Mismatches 2; Indels 0; Gaps 0;
 Matches 12; Conservative 24 RWCFRVCYRGICYRKCR 18
 DR Tachypleasin I.
 CC
 DR PIR: B39345; B39345.
 DR HSSP; P4213; IMA2.
 KW Amidation; Antibiotic; Cleavage on pair of basic residues;
 KW Direct protein sequencing; Signal.
 FT SIGNAL 1
 FT PEPTIDE 24 40 23
 FT PROPEP 41 77
 FT DISULFID 26 39
 FT DISULFID 30 35
 FT MOD_RES 40 40
 FT DOMAIN 69 77
 SQ SEQUENCE 77 AA; 9335 MW; 6EBB57AA652ABFF CRC64;
 Query Match 77.7%; Score 94; DB 1; Length 77;
 Best Local Similarity 76.5%; Pred. No. 6e-05; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 13; Conservative 24 RWCFRVCYRGICYRKCR 40
 DR PIR: JX0125; JX0125.
 DR HSSP; P4213; IMA2.
 KW Amidation; Antibiotic; Direct protein sequencing.
 KW Disulfide bond formation.
 CC -!- FUNCTION: Significantly inhibits the growth of Gram-negative and
 CC Gram-positive bacteria.
 CC -!- SUBCELLULAR LOCATION: S-granules.
 CC -!- TISSUE SPECIFICITY: Hemocytes.
 CC -!- SIMILARITY: Belongs to the tachypleasin/polyphemusin family.
 DR PIR: B39345; B39345.
 DR HSSP; P4213; IMA2.
 KW Amidation; Antibiotic; Cleavage on pair of basic residues;
 KW Direct protein sequencing; Signal.
 FT SIGNAL 1
 FT PEPTIDE 24 40 23
 FT PROPEP 41 77
 FT DISULFID 26 39
 FT DISULFID 30 35
 FT MOD_RES 40 40
 FT DOMAIN 69 77
 SQ SEQUENCE 77 AA; 9335 MW; 6EBB57AA652ABFF CRC64;
 Query Match 77.7%; Score 94; DB 1; Length 77;
 Best Local Similarity 76.5%; Pred. No. 6e-05; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 13; Conservative 24 RWCFRVCYRGICYRKCR 18
 DR Tachypleasin I.

OS Tachypleus gigas (Southeast Asian horseshoe crab), and
OS Carcinocorpius rotundicauda (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus;
OX NCBI_TaxID=6852, 6848;
RN SEQUENCE.
RP SPECIES=
RC S. rotundicauda, and T.gigas;
RX MEDLINE=9105357; PubMed=2229025;
RA Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
RT "tachypleins isolated from hemocytes of Southeast Asian horseshoe
Crabs (Carcinoscorpius rotundicauda and Tachypleus gigas):
identification of a new tachyplein, tachyplein III, and a processing
intermediate of its precursor.";
RL J. Biomed. 108:261-266(1990).
CC -!- SIMILARITY: Belongs to the tachyplein/polyphemusin family.
DR PIR: A38824; A38824.
DR PIR: JX0124; JX0124.
DR HSSP; P14213; IMA2.
KW Amidation; Antibiotic; Direct protein sequencing.
FT DISULFID 3 16
FT DISULFID 7 12
FT MOD RES 17 17 Arginine amide.
SQ SEQUENCE 17 AA; 2269 MW; E9E9BD9p292394 CRC64;
QV 2 RWCYRKCYKCYRKCR 18
Db 1 KWCFCRVCGICYRRCR 17

RESULT 6

TACI_TACTR	STANDARD:	PRT:	77 AA.
ID TACI_TACTR			
AC P14213;			
DT 01-JAN-1990 (Rel. 13, Created)			
DT 01-NOV-1991 (Rel. 20, Last sequence update)			
DT 25-OCT-2004 (Rel. 45, Last annotation update)			
DE Tachyplein I precursor.			
OS Tachypleus tridentatus (Japanese horseshoe crab).			
OC Bivalvia; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;			
OC Limulidae; Tachypleus;			
OX NCBI_TaxID=6853;			
RN SEQUENCE FROM N.A.			
RX MEDLINE=91065956; PubMed=2250028;			
RA Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; RT "Antimicrobial tachyplein peptide precursor: cDNA cloning and cellular localization in the horseshoe crab (Tachypleus tridentatus)." ;			
RL J. Biol. Chem. 265:21350-21354 (1990).			
RN [2]			
RP SEQUENCE OF 24-40, AND DISULFIDE BONDS.			
RX MEDLINE=890369158; PubMed=3141410;			
RA Nakamura T., Furukawa H., Miyata T., Tokunaga F., Muta T., Iwanaga S., NIWA M., TAKAO T., SHIMONISHI Y.;			
RT "Tachyplein, a class of antimicrobial peptide from the hemocytes of the horseshoe crab (Tachypleus tridentatus). Isolation and chemical structure." ;			
RL J. Biol. Chem. 263:16709-16713 (1988).			
RN [3]			
RP STRUCTURE BY NMR OF 24-40.			
RX MEDLINE=90369729; PubMed=2394727;			
RA Iwanaga S.; RT Antimicrobial peptide, tachyplein I, isolated from hemocytes of the horseshoe crab (Tachypleus tridentatus). NMR determination of the beta-sheet structure." ;			
RL J. Biol. Chem. 265:15365-15367 (1990).			
RN [4]			

RP STRUCTURE BY NMR OF 24-40.
RX MEDLINE=93257488; PubMed=8400053; DOI=10.1016/0167-4038(93)90183-R;
RA Tamamura H., Kuroda M., Masuda M., Okara A., Funakoshi S.,
Nakashima H., Yamamoto N., Waki M., Matsumoto A., Lancelein J.-M.,
RA Kohda D., Tate S., Inasaki F., Fujii N.,
RT "A comparative study of the solution structures of tachyplein I and a
novel anti-HIV synthetic peptide, T22 ([Tyr5,12, Lys7]-polyphemusin
II), determined by nuclear magnetic resonance.";
RL Biochim. Biophys. Acta 1163:209-216 (1993).
RN [5]

RP CHARACTERIZATION.

DR MEDLINE=94110249; PubMed=8282718;			
RA Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., ITO A., Iwanaga S.;			
RT "Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their components." ;			
RL J. Biomed. 114:307-316 (1993).			
CC FUNCTION: Significantly inhibits the growth of Gram-negative and Gram-positive bacteria.			
CC SUBCELLULAR LOCATION: S-granules.			
CC TISSUE SPECIFICITY: Hemocytes.			
CC SIMILARITY: Belongs to the tachyplein/polyphemusin family.			
CC			
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CC			
DR EMBL; DR			
DR PIR; A38345; A38345.			
DR PDB; IMA2; NMR; A24-40.			
DR PDB; IMA4; NMR; A24-40.			
DR PDB; IMA5; NMR; A24-40.			
DR PROBP; IMA6; NMR; A24-40.			
DR 3D-STRUCTURE: Amide bond cleavage on pair of basic residues; Direct protein sequencing; Signal.			
DR CLEAVAGE ON PAIR OF BASIC RESIDUES; DIRECT PROTEIN SEQUENCING; SIGNAL.			
FT SIGNAL 1 23			
FT PEPTIDE 24 40 Tachyplein I.			
FT PROBP 41 77			
FT DISULFID 26 39			
FT DISULFID 30 35			
FT MOD_RES 40 40 Arginine amide (G-41 provides amide group). Asp/Glu-rich (acidic).			
FT DOMAIN 69 77			
FT SEQUENCE 77 AA; 9349 MW; B940CAA41641335P CRC64;			
QV 2 RWCYRKCYKCYRKCR 18			
Db 24 KWCFCRVCGICYRRCR 40			

RESULT 7

OBNAK2	PRELIMINARY:	PRT:	398 AA.
ID OBNAK2			
AC OBNAK2;			
DT 01-OCT-2002 (TREMBrel 22, Created)			
DT 01-OCT-2002 (TREMBrel 22, Last sequence update)			
DT 01-MAR-2004 (TREMBrel 26, Last annotation update)			
DR Hypothetical Protein FLJ34633.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			

RC TISSUE=Kidney;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohayashi M.M., Nishi T., Shihara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahori K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamasaki M.,
 RA Niromiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraiwa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotota T., Kusano J.,
 RA Kanehori K., Takanashi F., Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Tojiga S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sakai N., Aotsuka S.,
 RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Tagashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano T.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45 (2004).
 DR EMBL; AR091952; BAC03775_1; -.
 SEQUENCE 398 AA; 43613 MW; BF1BD53D322A8D2 CRC64;

Query Match 44.6%; Score 54; DB 2; length 398;
 Best Local Similarity 38.9%; Pred. No. 33; Mismatches 7; Conservative 4; Indels 0; Gaps 0;

QY 1 RRWCYRKCKYCYRKCR 18
 ID 79 RPWVNEWCRAAFCFRRCR 96

RESULT 8

Q6CHR2 PRELIMINARY; PRT; 143 AA.

Q6CHR2 PRELIMINARY; PRT; 594 AA.

AC 024660 PRELIMINARY; PRT; 594 AA.

DT 024660; 01-JAN-1998 (TREMBREL 05; Created)
 DT 01-JAN-1998 (TREMBREL 05; Last sequence update)
 DT 05-JUL-2004 (TREMBREL 27; Last annotation update)

DE Transport inhibitor response 1 (TIR1) (Putative transport inhibitor
 DE response TIR1, AtTBLI protein); T20010-80;
 GN Name=TIR1; Synonyms=AtTBLI2900, T20010-80;

OS Arabidopsis thaliana (Mouse-ear cress);
 OC Butarvocae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids-II; Brassicales; Brassicaceae; Arabidopsis;
 OX NCBI_TaxID=3702; [1]

RP SEQUENCE FROM N.A.
 RA Rugger M., Dewey E., Gray B., Robbie L., Turner J., Estelle M.;
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Obermaier B., Ottewaelder B., Duchemin D., Zeitzer K., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X., Quettier F., Salanoubat M.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
 RA Ondera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
 RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
 RA Ecker J.R., Theologis A., Wick W.,
 RL Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR005048; ARB69176.1; -.

DR EMBL; AR005047; ARB69175.1; -.

DR EMBL; BY001946; IRR_CYS.

DR InterPro; IPR00180; F-box.

DR InterPro; IPR001611; IRR.

DR InterPro; IPR001609; IRR_CYS.

DR PIR; T48087; T48087.

DR IntAct; O24660; InterPro; IPR001810; F-box.

DR SMART; SM00266; FERÖX_1.

SQ SEQUENCE 594 AA; 66798 MW; 9B19ED5DABF40D07 CRC64;

Query Match 43.0%; Score 52; DB 2; Length 594;
 Best Local Similarity 61.5%; Pred. No. 85; 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RWCYRKCYKCYC 14
 ID 42 RWCRRKVFIGNCY 54

RESULT 10

Q7GR2 PRELIMINARY; PRT; 1040 AA.
 AC Q7GR2;
 DT 01-MAR-2004 (TREMBUREL 26, Created)
 DT 01-MAR-2004 (TREMBUREL 26, Last sequence update)
 DT 01-MAR-2004 (TREMBUREL 26, Last annotation update)
 DE WD_repeat protein p103.
 GN Name=PY04284;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1] SEQUENCE FROM N.A.

RC STAIN=TNLN;
 RX PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguilo S.V., Suh B.B., Kooij T.W., Pertea M.,
 RA Silva J.C., Emiolaava M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmiller S.B., Fieldlyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shaabi A., Cummings L.M.,
 RA Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaclav A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- SIMILARITY: Contains 8 WD repeats.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC preliminary genome shotgun (WGS) entry which is
 DR EMBL; ARBL01001288; EAA16119_1; "-".
 DR InterPro; IPR011045; N2O_reductase_N.
 DR InterPro; IPR011680; WD00.
 DR InterPro; IPR011046; WD00_like.
 DR Pfam; PF00400; WD40; 8.
 DR Prodrom; PD000018; WD40; 1.
 DR PROSITE; PS50082; WD_REPEATS_2; 2.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 3.
 SQ SEQUENCE 1040 AA; 119229 MW; RA6581547817C46C CRC64;
 SEQUENCE FROM N.A. AND AMINATION.
 Best Local Similarity 61.5%; Pred. No. 1.4e+02; 1; Mismatches 8; Conservative 8; Indels 2; Gaps 1; Matches 2.

Query Match 43.0%; Score 52; DB 2; Length 1040;
 Best Local Similarity 61.5%; Pred. No. 1.4e+02; 1; Mismatches 8; Conservative 8; Indels 2; Gaps 1; Matches 2.

QY 1 RWCYRKCYKCYC 13
 ID 277 KRWCYKKY--YC 287

RESULT 11

Q6V422 PRELIMINARY; PRT; 64 AA.
 AC Q6V422;
 DT 05-JUL-2004 (TREMBUREL 27, Created)
 DT 05-JUL-2004 (TREMBUREL 27, Last sequence update)
 DT 05-JUL-2004 (TREMBUREL 27, Last annotation update)
 DE Beta-toxin (Fragment).
 OS Centruroides noxius (Mexican scorpion).
 OC Buthida; Metazoa; Arthropoda; Chelicerrata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Centruroides.

OX NCBI_TaxID=6878;
 RN [1] SEQUENCE FROM N.A.

RA Zhu S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 RL -!- SUBCELLULAR LOCATION: Secreted (By/ Similarity).
 CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
 DR EMBL; AX51298; AACR08033.1; -.
 DR HSSP; P01491; 1B3C.
 DR GO; GO:0005576; C:extracellular; F:ion channel inhibitor activity; IEA.
 DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0006932; F:defense response; IEA.
 DR GO; GO:0009405; P:pathogenetis; IBA.
 DR InterPro; IPR03614; Knot1.
 DR InterPro; IPR01219; Neurotoxin.
 DR InterPro; IPR02051; Scorpion_toxinL.
 DR Pfam; PF00537; Toxin 3; 1.
 DR PRINTS; PR0085; SCORPNTOXIN.
 DR PRINTS; PR00214; TOXIN.
 DR ProDom; PD000908; Scorpion_toxinL; 1.
 DR SMART; SM00505; Knot1; 1.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 64 AA; 7248 MW; 082F5D9512A289FD CRC64;
 SEQUENCE FROM N.A. AND AMINATION.
 ID SCX1_CENNO STANDARD; PRT; 86 AA.
 AC P15223; CENNO_2024640;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-2004 (Rel. 44, Last annotation update)
 DE Toxin 1 precursor (Toxin II 14) (Cn1).
 OS Centruroides noxius (Mexican Scorpion).
 OC Buthida; Buthoidea; Buthidae; Centruroides.
 OX NCBI_TaxID=6878;
 RN [1] SEQUENCE FROM N.A. AND AMINATION.
 DR MEDLINE=96119048; PubMed=8550086; DOI=10.1016/0041-0101(95)00058-T;
 RA Vazquez A., Tapia J.V., Elision W.K., Martin B.M., Lebreton F.,
 RA Delpierre M., Possani L.D., Berrill B.;
 RT "Cloning and characterization of the cDNAs encoding Na⁺ channel-specific toxins 1 and 2 of the scorpion Centruroides noxius Hoffmann,"; Hoffmann, R., Toxicon 33:1161-1170(1995).
 RT Hoffmann, R., Toxicon 33:1161-1170(1995).
 RN [2] SEQUENCE OF 20-84.
 RC TISSUE=Venom;
 RX MEDLINE=86025386; PubMed=4052021;
 RA Possani L.D., Martin B.M., Svendsen I., Rode G.S., Erickson B.W.;
 RT "Scorpion toxins from Centruroides noxius and *Tityus serrulatus*. Primary structures and sequence comparison by metric analysis.";
 RL Biochem. J. 229:739-750(1985).
 CC -!- FUNCTION: Binds voltage-independent at site 4 of sodium channels and shift the voltage of activation toward more negative potentials.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-toxin subfamily.
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DR InterPro; IPR001219; Neurotoxin.

DR InterPro; IPR00261; Scorpion_toxinL.

DR Pfam; PF00537; Toxin_3_1.

DR PRINTS; PRO0285; SCORPNTOXIN.

DR PRODom; PD00908; Scorpion_toxinL_1.

DR PRODom; PD00908; Scorpion_toxinL_1.

DR KWLAmidation; Direct_protein_sequencing; Ionic_channel_inhibitor;

DR KWLNeurotoxin; Signal; Sodium_channel_inhibitor; Toxin.

DR SIGNAL 1

FT CHAIN 20

FT DISULFID 30

FT DISULFID 34

FT DISULFID 43

FT DISULFID 47

FT MOD_RES 84

FT CONFLICT 79

FT CONFLICT 79

FT SEQUENCE 86 AA; 9586 MW; AB8C1EA742F17222 CRC64;

Query Match 42.1%; Score 51; DB 1; Length 86;
 Best Local Similarity 47.4%; Pred. No. 21;
 Matches 9; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 4 CYRKCYK---GYCYRKCR 18

Db 30 CKKNCKYLGNDDYCNR 48

RESULT 13

ID 06ZZP9 PRELIMINARY; PRT; 83 AA.

AC 06ZZP9; Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DR Putative trypsin inhibitor 3;

DR Name=ATR13; ORFNames=At2g43530;

DR Arabidopsis thaliana (Mouse-ear cress).

DR Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

DR Spermatophyta; Magnoliophyta; eudicots; rosids;

DR eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID:3702;

RN [1]

RP SEQUENCE FROM N.A.

RT TISSUE=leaf;

RX Pubmed=15082560; DOI=10.1534/genetics.166.3.1419;

RA Claus M.J., Mitchell-Olds T.;

RT "Functional divergence in tandemly duplicated Arabidopsis thaliana trypsin inhibitor"; Genetics 166:1419-1436 (2004).

DR Genes 166:1419-1436 (2004).

DR HSSP; Q82328; 1JJC.

DR InterPro; IPR00261; Scorpion_toxinL.

DR Pfam; PF00537; Toxin_3_1.

DR SMART; SW00505; Knotl_1.

DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; UNKNOWN_1.

DR SEQUENCE 83 AA; 9424 MW; BDA24E6A1290F93E CRC64;

Query Match 41.3%; Score 50; DB 2; Length 83;
 Best Local Similarity 43.8%; Pred. No. 28;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 WCYRKCYKCYRKCR 18

Db 43 YCMARIYPSLCYRNCR 58

RP SEQUENCE FROM N.A.

RC TISSUE=leaf;

RX PubMed=15082560; DOI=10.1534/genetics.166.3.1419;

RA Claus M.J., Mitchell-Olds T.;

RT "Functional divergence in tandemly duplicated Arabidopsis thaliana trypsin inhibitor.";

RT "Genes 166:1419-1436 (2004)."

RL Genes 166:1419-1436 (2004).

DR EMBL; Ad632259; CAGI5205_1; -.

DR EMBL; Ad632250; CAGI5157_1; -.

DR HSSP; Q42328; 1JJC.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0008200; F:ion_channel_inhibitor_activity; IEA.

DR GO; GO:0009452; P:defense_response; IEA.

DR InterPro; IPR01542; Defensin_anped.

DR InterPro; IPR003614; Knotl_1.

DR InterPro; IPR002061; Scorpion_toxinL.

DR Pfam; PF00537; Toxin_3_1.

DR SMART; SM00505; Knotl_1.

DR SEQUENCE 83 AA; 9408 MW; A7130584F290F934 CRC64;

RX PubMed=15082560; DOI=10.1534/genetics.166.3.1419;

Query Match 41.3%; Score 50; DB 2; Length 83;
 Best Local Similarity 43.8%; Pred. No. 28;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 WCYRKCYKCYRKCR 18

Db 43 YCMARIYPSLCYRNCR 58

RESULT 15

ID 06ZZQ9 PRELIMINARY; PRT; 83 AA.

AC 06ZZQ9; Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DR Putative trypsin inhibitor 3.

DR Name=ATR13; ORFNames=At2g43530;

DR Arabidopsis thaliana (Mouse-ear cress).

DR Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

DR Spermatophyta; Magnoliophyta; eudicots; rosids;

DR eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID:3702;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=leaf;

RX PubMed=15082560; DOI=10.1534/genetics.166.3.1419;

RT		"Functional divergence in tandemly duplicated <i>Arabidopsis thaliana</i> trypsin inhibitor.";
RL	Genetics 166:1419-1436(2004)	
DR	EMBL; AJ632257; CAG15195.1; -	
DR	EMBL; AU632260; CAG15210.1; -	
DR	EMBL; AJ632261; CAG15215.1; -	
DR	EMBL; AJ632262; CAG15220.1; -	
DR	EMBL; AU632263; CAG15225.1; -	
DR	EMBL; AJ632264; CAG15230.1; -	
DR	EMBL; AJ632265; CAG15235.1; -	
DR	EMBL; AU632266; CAG15240.1; -	
DR	HSSP; Q42328; 1JXC.	
DR	GO; GO:000556; C:extracellular; IEA.	
DR	GO; GO:000820; R:ion channel inhibitor activity; IEA.	
DR	GO; GO:006552; P:pathogen response; IEA.	
DR	GO; GO:009405; P:pathogenesis; IEA.	
DR	InterPro; IPR01542; Defensin_apoid.	
DR	InterPro; IPR03614; Knottin.	
DR	InterPro; IPR02061; Scorpion_toxinN.	
DR	Pfam; PF00537; Toxin_3_1.	
DR	SMART; SM00505; Knottin_1.	
DR	PROSITE; PS00425; ARTHROPOD_DEFENSINS; UNKNOWN ¹ .	
SQ	SEQUENCE 83 AA; 9348 MW; B3424084290FF334 CRG64;	
Query	Match	41.3%; Score 50; DB 2; length 83;
Best Local Similarity	43.8%	Pred. No. 28;
Matches	7;	Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY	3 WCYRKCKGKSYCYRKCR 18	
Db	: :	
Db	43 YCMARRIYPSLICYRNCR 58	

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OM protein - protein search, using SW model

Run on: May 9, 2005, 20:58:48 ; Search time 164 Seconds
(without alignments)
42.419 Million cell updates/sec

Title: US-10-706-265-2

Perfect score: 121

Sequence: 1 RRCYRKCYKCYRKCR 18

Scoring table: BL0SUM62

Gapext 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqD1980s:*

2: geneseqD1990s:*

3: geneseqD2000s:*

4: geneseqD2001s:*

5: geneseqD2002s:*

6: geneseqD2003aa:*

7: geneseqD2003bs:*

8: geneseqD2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	121	AAW37578	2	AAW37578	Aaw37578 Synergist
2	121	AAW40570	2	AAW40570	Aaw40570 PolyPeptid
3	121	AAW40561	2	AAW40561	Aaw40561 PolyPeptid
4	100	AAW79839	2	AAW79839	Aaw79839 Peptide s
5	121	AAB9844	4	AAB9844	Aab9844 Antimicro
6	100	ADQ1480	8	ADQ1480	Adq1480 Metastabi
7	121	AAW28775	2	AAW28775	Aaw28775 High endo
8	121	AAW3579	2	AAW3579	Aaw3579 Synergist
9	121	AAW9840	2	AAW9840	Aaw9840 Peptide s
10	118	AAW28785	2	AAW28785	Aaw28785 High endo
11	118	AAW3591	2	AAW3591	Aaw3591 Synergist
12	118	AAW9852	2	AAW9852	Aaw9852 Peptide s
13	117	AAW28784	2	AAW28784	Aaw28784 High endo
14	117	AAW3590	2	AAW3590	Aaw3590 Synergist
15	117	AAW9851	2	AAW9851	Aaw9851 Peptide s
16	116	AAW28793	2	AAW28793	Aaw28793 High endo
17	116	AAW33603	2	AAW33603	Aaw33603 Synergist
18	116	AAW79864	2	AAW79864	Aaw79864 Peptide s
19	116	AAW79843	2	AAW79843	Aaw79843 Peptide s
20	115	AAW28781	2	AAW28781	Aaw28781 High endo
21	115	AAW28792	2	AAW28792	Aaw28792 High endo
22	115	AAW37586	2	AAW37586	Aaw37586 Synergist
23	115	AAW79847	2	AAW79847	Aaw79847 Peptide s
24	115	AAW79863	2	AAW79863	Aaw79863 Peptide s
25	114	AAW28799	2	AAW28799	Aaw28799 High endo

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : AAW37578 standard; peptide; 18 AA.

AC AAW37578;

XX DT 10-MAR-1998 (first entry)

XX DB Synergistic HIV enzyme inhibitor enhancing peptide (23).

XX KW Human immunodeficiency virus; HIV; reverse transcriptase; protease; inhibitor; antiviral; synergistic enhancer.

XX OS Synthetic.

XX FH Key Disulfide-bond /note= "optional"

FT FT Location/Qualifiers

FT FT Modified-site 18 /note= "amidated"

FT XX /note= "amidated"

FT PN JP09025240-A.

XX PD 28-JAN-1997.

XX PP 11-JUL-1995; 95JP-00197129.

XX PR 11-JUL-1995; 95JP-00197129.

XX PA (SEGK) SEIKAGAKU KOGYO CO LTD.

XX DR WPI: 1997-14971/14.

XX PT Antiviral compsn. against human immunodeficiency virus - contg. specified

PT polyPeptide and HIV reverse transcriptase inhibitor or HIV protease

PT inhibitor.

XX PS Example: Page 6; 13pp; Japanese.

XX CC A novel medicinal composition, comprising the present peptide and a human immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor, can be used as an antiviral drug. The composition is highly active against HIV, and can be administered over a long period. The dose of the HIV enzyme inhibitor can be reduced, because combined use with the present peptide synergistically enhances its antiviral activity

CC Sequence 18 AA;

SQ

26	114	94.2	18	2	AAW37610 Synergist
27	114	94.2	18	2	Aaw9871 Peptide s
28	113	93.4	17	2	Aaw37592 Synergist
29	113	93.4	17	2	Aaw79853 Peptide s
30	113	93.4	18	2	Aar22535 Anti-HIV
31	113	93.4	18	2	Aar22536 Anti-HIV
32	113	93.4	18	2	Aaw37565 Synergist
33	113	93.4	18	2	Aaw37563 Synergist
34	113	93.4	18	2	Aaw37597 Synergist
35	113	93.4	18	2	Aaw40566 PolyPepti
36	113	93.4	18	2	Aaw0565 PolyPepti
37	113	93.4	18	2	Aaw79858 Peptide s
38	113	93.4	18	2	Aaw79826 Peptide s
39	113	93.4	18	2	Aaw79824 Peptide s
40	113	93.4	19	2	Aar28789 High endo
41	113	93.4	19	2	Aaw37599 Synergist
42	113	93.4	19	2	Aaw19860 Peptide s
43	112	92.6	17	2	Aaw79850 Synergist
44	112	92.6	17	2	Aaw79841 Peptide s
45	112	92.6	18	2	Aar28776 High endo

ALIGNMENTS

Query Match 100.0%; Score 121; DB 2; Length 18;
 Best Local Similarity 100.0%; Prd. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRWCYRKCYKGYCYRKCR 18
 AC XX
 AC AAW40570;
 AC XX
 DT 27-AUG-1998 (first entry)
 DE Polypeptide transition metal peptide fragment.
 XX
 KW Polypeptide transition metal salt; inhibition; viral activity; HIV.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1 /note= "labelled with FTC"
 FT XX
 PN WO9816555-A1.
 XX
 PD 23-APR-1998.
 XX
 PR 15-OCT-1997; 97WO-JP003711.
 XX
 PA (SISGK) SEIKAGAKU CORP.
 XX
 PI Matsumoto A, Waki M;
 XX
 DR WPI: 1998-251233/22.
 XX
 PT Polypeptide transition metal salt or its acid adduct - useful for
 PT inhibiting viral activity, e.g. HIV in vivo.
 XX
 PD Disclosure; Page 6; 45pp; Japanese.
 XX
 CC AAW40561-70 represent fragments of a polypeptide transition metal salt or
 its acid adduct. The peptides comprise the formula: A1-A2-Cys-A2-A3-A3-X-
 Y-Z-A2-A3-A3-Cys-A3-A4 where A1 = Lys, Arg or Orn, optionally N- alpha
 substituted or peptide comprising at least 2 of these residues,
 optionally N- alpha substituted; A2 = Phe, Trp or Tyr; A3 = Arg, Lys or
 Met or Cys bound to A1; Y = dipeptide comprising Ala, Val, Leu, Ile, Ser,
 Arg, D-Lys or D-Orn, and Z = dipeptide comprising Gly and A3 or Pro, D-
 Ser, Met or A2 bound to Cys, or the peptide bond linked X-Y-Z have
 peptide bonds to other aa at positions 6 and 10, or if neither X nor Z
 exist, then Y may bond to them directly, in which case the D-Lys, L-Lys,
 D-Orn or L-Orn of Y may be substituted by omega -aminoacyl. The salt may
 be used for inhibiting viral activity, and is especially useful against
 HIV in vivo
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 121; DB 2; Length 18;
 Best Local Similarity 100.0%; Prd. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRWCYRKCYKGYCYRKCR 18
 AC XX
 AC AAW79839;
 AC XX
 DT 08-DEC-1998 (first entry)
 DE Peptide sequence of the specification.
 XX
 KW Reverse-transcriptase inhibitor; HIV protease inhibitor;
 KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;
 KW AIDS-associated syndrome.
 XX
 OS Synthetic.

RESULT 2
 ID AAW40570 standard; peptide; 18 AA.
 XX
 ID AAW40561 standard; peptide; 18 AA.
 XX
 ID AAW40561;
 XX
 DT 27-AUG-1998 (first entry)
 DE Polypeptide transition metal peptide fragment.
 XX
 KW Polypeptide transition metal salt; inhibition; viral activity; HIV.
 OS Synthetic.

XX
 PN WO9816555-A1.
 XX
 PD 23-APR-1998.
 XX
 PR 15-OCT-1997; 97WO-JP003711..
 XX
 PR 15-OCT-1996; 96JP-00291215.
 XX
 PA (SISGK) SEIKAGAKU CORP.
 XX
 PI Matsumoto A, Waki M;
 XX
 DR WPI: 1998-251233/22.
 XX
 PT Polypeptide transition metal salt or its acid adduct - useful for
 PT inhibiting viral activity, e.g. HIV in vivo.
 XX
 PD Disclosure; Page 6; 45pp; Japanese.
 XX
 CC AAW40561-70 represent fragments of a polypeptide transition metal salt or
 its acid adduct. The peptides comprise the formula: A1-A2-Cys-A2-A3-A3-X-
 Y-Z-A2-A3-A3-Cys-A3-A4 where A1 = Lys, Arg or Orn, optionally N- alpha
 substituted or peptide comprising at least 2 of these residues,
 optionally N- alpha substituted; A2 = Phe, Trp or Tyr; A3 = Arg, Lys or
 Orn; A4 = -OH or -NH2; X = dipeptide comprising Ala, Val, Leu, Ile, Ser,
 Met or Cys bound to A1; Y = dipeptide comprising Gly and A3 or Pro, D-
 Arg, D-Lys or D-Orn, and Z = dipeptide comprising Ala, Val, Leu, Ile,
 Ser, Met or A2 bound to Cys, or the peptide bond linked X-Y-Z have
 peptide bonds to other aa at positions 6 and 10, or if neither X nor Z
 exist, then Y may bond to them directly, in which case the D-Lys, L-Lys,
 D-Orn or L-Orn of Y may be substituted by omega -aminoacyl. The salt may
 be used for inhibiting viral activity, and is especially useful against
 HIV in vivo
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 121; DB 2; Length 18;
 Best Local Similarity 100.0%; Prd. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRWCYRKCYKGYCYRKCR 18
 AC XX
 AC AAW79839;
 AC XX
 DT 08-DEC-1998 (first entry)
 DE Peptide sequence of the specification.
 XX
 KW Reverse-transcriptase inhibitor; HIV protease inhibitor;
 KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;
 KW AIDS-associated syndrome.
 XX
 OS Synthetic.

RESULT 3
 OS

PT peptidase degradation, useful for increasing length of in vivo activity.

XX WO9843995-A1.

PN XX

XX PT

XX PS

XX Disclosure; Page 529; 733pp; English.

XX PD 08-OCT-1998.

XX XX

XX PF 26-MAR-1998; 98W0-JP001366.

PR XX 28-MAR-1997; 97JP-00092801.

PA XX (SGK) SEIKAGAKU CORP.

XX PT Fujii N;

XX DR WPI; 1998-542630/46.

XX PT New therapeutic compositions comprise anti-HIV complexes - useful for

PT homing drug substance to target cells to enhance anti-HIV activity, for

PT treatment of AIDS.

XX Disclosure; Page 10; 44pp; Japanese.

CC AAW79817-85 appear in the specification. The specification describes

CC complexes which comprise at least one reverse-transcriptase inhibitor

CC and/or HIV protease inhibitor chemically bonded to polypeptides with an

CC affinity for HIV surface protein gp120 and/or HIV host target cell

CC surface protein CD4. The complexes can be used to prepare therapeutics

CC for treatment of AIDS and AIDS-associated syndromes

XX Sequence 18 AA;

Query Match 100.0%; Score 121; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 18; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRWCKRKCKGCKRKCR 18

Db 1 RRWCYRKCKGCKRKCR 18

RESULT 5

ID AAB91844

ID AAB91844 standard; Peptide; 18 AA.

XX AC AAB91844;

XX DT 22-JUN-2001 (first entry)

XX DB Antimicrobial peptide SEQ ID NO:1020.

XX OS Homo sapiens.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimidyl; maleimido group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Synthetic.

XX US2004132642-A1.

PN 08-JUL-2004.

XX PR 12-NOV-2003; 2003US-00706265.

XX PR 12-NOV-2002; 2002US-0425472B.

XX PR 15-OCT-2003; 2003US-0511581P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PT Hwang S;

XX DR WPI; 2004-517028/49.

XX PT Use of a polypeptide that inhibits metastasis of tumor cells, which

PT expresses CXCR Chemokine Receptor-4, for inhibiting metastasis or growth

PT of a tumor cell.

XX PS Claim 2; SEQ ID NO 2; 31pp; English.

XX CC The invention describes the use of a polypeptide that inhibits metastasis

CC of tumor cells, where the tumor cell expresses CXCR Chemokine Receptor-4

CC (CXCR4), for inhibiting metastasis or growth of a tumor cell. Also

CC Modifying and attaching therapeutic peptides to albumin prevents

PR 02-MAY-1991; 91JP-00130410.
 XX
 DE Peptide sequence of the specification.
 XX
 KW Reverse-transcriptase inhibitor; HIV protease inhibitor;
 KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;
 KW AIDS-associated syndrome.
 XX
 OS Synthetic.
 XX
 PN WO9843995-A1.
 XX
 PD 08-OCT-1998.
 XX
 PR 26-MAR-1998; 98WO-JP001366.
 XX
 PT 28-MAR-1997; 97JP-00092801.
 XX
 PA (SEIGK) SEIKAGAKU CORP.
 Fujii N,
 PI
 XX
 DR WPI; 1998-542630/46.
 XX
 PT New therapeutic compositions comprise anti-HIV complexes - useful for
 PT homing drug substance to target cells to enhance anti-HIV activity, for
 PT treatment of AIDS.
 XX
 PS Disclosure; Page 10; 44pp; Japanese.
 XX
 CC AAM79817-85 appear in the specification. The specification describes
 CC complexes which comprise at least one reverse-transcriptase inhibitor
 CC and/or HIV protease inhibitor chemically bonded to polypeptides with an
 CC affinity for HIV surface protein gp120 and/or HIV host target cell
 CC surface protein CD4. The complexes can be used to prepare therapeutics
 CC for treatment of AIDS and AIDS-associated syndromes
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 121; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07; Mismatches 0;
 Matches 18; Conservative 0; Indels 0; Gaps 0;
 AC
 Qy 1 RRWCYRKCYKGYCYRKCR 18
 1 RRWCYRKCYKGYCYRKCR 18
 Db
 1 RRWCYRKCYKGYCYRKCR 18
 XX
 RESULT 10
 AAR28785
 ID AAR28785 standard; peptide; 18 AA.
 XX
 AC AAR28785;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-MAR-1993 (first entry)
 DE High endotoxin affinity polypeptide.
 XX
 KW Lipopolysaccharide affinity; tachypleasin-like; polyphemusin-like;
 KW antiviral activity; HIV; human immunodeficiency virus.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site
 FT Disulfide-bond
 FT
 FT
 FT
 PN JP09025240-A.
 XX
 PD 28-JAN-1997.
 XX
 PR 11-JUL-1995; 95JP-00197129.
 XX
 PR 11-JUL-1995; 95JP-00197129.
 XX
 PA (SEIGK) SEIKAGAKU KOGYO CO LTD.
 XX
 DR WPI; 1997-149771/14.
 XX
 PT Antiviral compn. against human immunodeficiency virus - contg. specified
 PT polypeptide and HIV reverse transcriptase inhibitor or HIV protease
 PT inhibitor.
 XX
 PN EP513613-A1.
 XX
 PD 19-NOV-1992.
 XX
 PT 04-MAY-1992; 92EP-00107509.
 XX

PS Example; Page 7; 13pp; Japanese.

XX A novel medicinal composition, comprising the present peptide and a human immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor, can be used as an antiviral drug. The composition is highly active against HIV, and can be administered over a long period. The dose of the HIV enzyme inhibitor can be reduced, because combined use with the present peptide synergistically enhances its antiviral activity.

XX Sequence 18 AA;

Query Match 97.5%; Score 118; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 4e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCYRKCKGKCYRKCR 18
Db 1 RRWCYRKCKGKCYRKCR 18

RESULT 12
AAW79852 standard; peptide; 18 AA.
ID AAW79852;
XX AC AAW79852;
XX DT 08-DEC-1998 (first entry)
DE Peptide sequence of the specification.
XX Reverse-transcriptase inhibitor; HIV protease inhibitor;
KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;
KW AIDS-associated syndrome.
OS Synthetic.
XX PN W09843995-A1.
XX PD 08-OCT-1998.
XX PF 26-MAR-1998; 98WO-JP001366.
XX PR 28-MAR-1997; 97JP-00092801.
PA (SRGK) SEIKAGAKU CORP.
XX PI Fujii N;
XX DR WPI; 1992-333533/47.
XX PT New tachypleasin- and polyphemusin-like polypeptide(s) - have endotoxin-binding activity, antibacterial activity and antiviral activity, partic. anti-HIV activity.
XX PS Disclosure; Page 4; 17pp; English.
XX CC The polypeptide has an ability to bind endotoxins, an antibacterial activity and an activity to haemolyse endotoxin-sensitized haemocytes. It also has antiviral activity, specifically anti-HIV activity. It exhibits higher anti-HIV activity than known related high endotoxin affinity polypeptides, e.g. Tachypleasin I, II or III or Polyphemusin I or II. It may be prepared by solid phase synthesis or recombinant DNA techniques. Opt. the Cys residues at positions 4 and 17 are linked through a disulphide linkage as are the Cys residues at positions 8 and 13. See also AAR28775-R28799 and AAR28804. (Updated on 25-MAR-2003 to correct PN field.)
XX PS Disclosure; Page 11; 4pp; Japanese.

XX AAW79817-85 appear in the specification. The specification describes complexes which comprise at least one reverse-transcriptase inhibitor and/or HIV protease inhibitor chemically bonded to polypeptides with an affinity for HIV surface protein gp120 and/or HIV host target cell surface protein CD4. The complexes can be used to prepare therapeutics for treatment of AIDS and AIDS-associated syndromes Sequence 18 AA.

Query Match 96.7%; Score 117; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.2e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCYRKCKGKCYRKCR 18
Db 1 RRWCYRKCKGKCYRKCR 18

RESULT 13
AAR28784 standard; peptide; 18 AA.
ID AAR28784
XX AC AAR28784;
XX DT 25-MAR-2003 (revised)
DT 23-MAR-1993 (first entry)
XX DE High endotoxin affinity polypeptide.
XX KW Lipopolysaccharide affinity; tachypleasin-like; polyphemusin-like; antiviral activity; HIV; human immunodeficiency virus.
XX OS Synthetic.
XX FH Key Modified-site 18 Location/Qualifiers /note= "Arg-NH2"
FT FT
XX PN EP513613-A1.
XX PD 19-NOV-1992.
XX PF 04-MAY-1992; 92EP-00107509.
XX PR 02-MAY-1991; 91JP-00130410.
XX PA (SRGK) SEIKAGAKU KOGYO CO LTD.
XX PI Fujii N, Yamamoto N, Matsumoto A, Waki M;
XX DR WPI; 1992-333533/47.
XX PT New tachypleasin- and polyphemusin-like polypeptide(s) - have endotoxin-binding activity, antibacterial activity and antiviral activity, partic. anti-HIV activity.
XX PS Disclosure; Page 4; 17pp; English.
XX CC The polypeptide has an ability to bind endotoxins, an antibacterial activity and an activity to haemolyse endotoxin-sensitized haemocytes. It also has antiviral activity, specifically anti-HIV activity. It exhibits higher anti-HIV activity than known related high endotoxin affinity polypeptides, e.g. Tachypleasin I, II or III or Polyphemusin I or II. It may be prepared by solid phase synthesis or recombinant DNA techniques. Opt. the Cys residues at positions 4 and 17 are linked through a disulphide linkage as are the Cys residues at positions 8 and 13. See also AAR28775-R28799 and AAR28804. (Updated on 25-MAR-2003 to correct PN field.)
XX PS Disclosure; Page 11; 4pp; Japanese.

XX AAW79817-85 appear in the specification. The specification describes complexes which comprise at least one reverse-transcriptase inhibitor and/or HIV protease inhibitor chemically bonded to polypeptides with an affinity for HIV surface protein gp120 and/or HIV host target cell surface protein CD4. The complexes can be used to prepare therapeutics for treatment of AIDS and AIDS-associated syndromes Sequence 18 AA.

Query Match 96.7%; Score 117; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.2e-07; Mismatches 1; Indels 0; Gaps 0;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCYRKCKGKCYRKCR 18
Db 1 RRWCYRKCKGKCYRKCR 18

RESULT 14
AAN37590 standard; peptide; 18 AA.
ID AAN37590
XX AC AAN37590;
XX DT 10-MAR-1998 (first entry)
XX DE Synergistic HIV enzyme inhibitor enhancing peptide (35).

KW Human immunodeficiency virus; HIV; reverse transcriptase; protease;
 KW inhibitor; antiviral; synergistic enhancer.
 XX
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT Disulfide-bond 4..17 /note= "optional"
 FT 18 /note= "amidated"
 XX
 PN JPO9025240-A.
 XX
 PD 28-JAN-1997.
 XX
 PR 11-JUL-1995; 95JP-00197129.
 XX
 PR 11-JUL-1995; 95JP-00197129.
 XX
 PA (SEIGAKU) SEIKAGAKU KOGYO CO LTD.
 XX
 DR WPI; 1997-14971/14.
 XX
 PT Antiviral compsn. against human immunodeficiency virus - contg. specified
 PT polypeptide and HIV reverse transcriptase inhibitor or HIV protease
 PT inhibitor.
 XX
 PS Example; Page 7; 13pp; Japanese.
 XX
 CC A novel medicinal composition, comprising the present peptide and a human
 CC immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor,
 CC can be used as an antiviral drug. The composition is highly active
 CC against HIV, and can be administered over a long period. The dose of the
 CC HIV enzyme inhibitor can be reduced, because combined use with the
 CC present peptide synergistically enhances its antiviral activity
 XX
 SQ Sequence 18 AA;
 Query Match 96.7%; Score 117; DB 2; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.2e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCYRKCYKGFCYRKCR 18
 |||||:|||||:|||||:
 Db 1 RRWCYRKCYKGFCYRKCR 18
 |||||:|||||:
 1 RRWCYRKCYKGFCYRKCR 18
 XX
 RESULT 15
 AAW79851
 ID AAW79851 standard; peptide; 18 AA.
 XX
 AC AAW79851;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE Peptide sequence of the specification.
 XX
 KW Reverse-transcriptase inhibitor; HIV protease inhibitor;
 KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;
 KW AIDS-associated syndrome.
 XX
 OS Synthetic.
 XX
 PN WO9843995-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 26-MAR-1998; 98WO-JP001366.
 XX
 PR 28-MAR-1997; 97JP-00092801.
 XX
 PA (SEIGAKU) SEIKAGAKU CORP.
 XX

PI Fuji N;
 XX
 DR WPI; 1998-542630/46.
 XX
 PT New therapeutic compositions comprise anti-HIV complexes - useful for
 PT honing drug substance to target cells to enhance anti-HIV activity, for
 PT treatment of AIDS.
 XX
 PS Disclosure; Page 11; 44pp; Japanese.
 XX
 CC AAW79817-85 appear in the specification. The specification describes
 CC complexes which comprise at least one reverse-transcriptase inhibitor
 CC and/or HIV protease inhibitor chemically bonded to polypeptides with an
 CC affinity for HIV surface protein gp120 and/or HIV host target cell
 CC surface protein CD4. The complexes can be used to prepare therapeutics
 CC for treatment of AIDS and AIDS-associated syndromes
 XX

SQ Sequence 18 AA;
 Query Match 96.7%; Score 117; DB 2; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.2e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCYRKCYKGFCYRKCR 18
 |||||:|||||:
 Db 1 RRWCYRKCYKGFCYRKCR 18
 |||||:
 1 RRWCYRKCYKGFCYRKCR 18

Search completed: May 9, 2005, 21:14:26
 Job time : 105 secs

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GenCore version 5.1.6

Run on: May 9, 2005, 21:07:54 ; Search time 42 Seconds
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Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/iaa/5B_COMB_pep: *
- 3: /cgn2_6/prodata/1/iaa/6A_COMB_pep: *
- 4: /cgn2_6/prodata/1/iaa/6B_COMB_pep: *
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB_pep: *
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	121	100.0	18	US-07-876-883-7
2	121	100.0	18	US-08-426-550-7
3	121	100.0	18	US-09-284-281-1
4	121	100.0	19	US-07-876-883-8
5	121	100.0	19	US-08-426-550-8
6	118	97.5	18	US-07-876-883-20
7	118	97.5	18	US-08-426-550-20
8	117	96.7	18	US-07-876-883-19
9	117	96.7	18	US-08-426-550-19
10	116	95.9	17	US-07-876-883-32
11	116	95.9	17	US-08-426-550-32
12	115	95.0	18	US-07-876-883-15
13	115	95.0	18	US-07-876-883-31
14	115	95.0	18	US-08-426-550-15
15	115	95.0	18	US-08-426-550-31
16	114	94.2	18	US-07-876-883-39
17	114	94.2	18	US-08-426-550-39
18	113	93.4	17	US-07-876-883-21
19	113	93.4	17	US-08-426-550-21
20	113	93.4	18	US-07-876-883-26
21	113	93.4	18	US-07-856-026B-9
22	113	93.4	18	US-07-856-026B-11
23	113	93.4	18	US-08-426-550-26
24	113	93.4	18	US-09-284-211-4
25	113	93.4	19	US-07-876-883-28
26	113	93.4	19	US-08-426-550-28
27	92.6	17	US-07-876-883-9	

ALIGNMENTS

RESULT 1
 US-07-876-883-7
 Sequence 7, Application US/07876883
 Patent No. 5449752

GENERAL INFORMATION:

APPLICANT: Fujii, No. 5449752utaka
 APPLICANT: Yamamoto, Akiyoshi
 APPLICANT: Wakai, Michinori
 APPLICANT: Matsumoto, Akiyoshi

TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To Lipopolysaccharides And Their Uses

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penne & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/876,883
 FILING DATE: 1990/04/29
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,575
 REFERENCE/DOCKET NUMBER: 7556-003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9050
 TELEFAX: 212 869-9741
 TELIX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: AMINO ACID
 STRANDBNESS: Single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-07-876-883-7

Query Match Score 100%; DB 1; Length 18;
 Best Local Similarity 100%; Pred. No. 1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMCYRKYKGCKRCA 18

Db 1 |||||RRWCYRKCYKGYCYRKCR 18

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence

RESULT 2
Sequence 7, Application US/08426550
Patient No. 5710128

GENERAL INFORMATION:
APPLICANT: Fuji, No. 5710128utaka

APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi

APPLICANT: Waki, Michinori

TITLE OF INVENTION: Pharmaceutical Compositions of
TITLE OF INVENTION: Pharmaceutical Compositions of
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550

FILING DATE: 21-APR-1995
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.

REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08426-550-7

Query Match Best Local Similarity 100.0%; Pred. No. 1e-08; Length 18; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMWYRKCKYKGYCYRKCR 18

Db 1 RRWCYRKCYKGYCYRKCR 18

RESULT 3
US-09-284-241-1

Sequence 1, Application US/09284241B
Patient No. 6329498

GENERAL INFORMATION:
APPLICANT: MATSUMOTO, AKIYOSHI

APPLICANT: WAKI, MICHINORI

TITLE OF INVENTION: ENHANCING ANTI-HIV ACTIVITY OF POLYPEPTIDE
FILE REFERENCE: 9378-005-0PCT

CURRENT APPLICATION NUMBER: US/09/284,241B

CURRENT FILING DATE: 1999-04-14

EARLIER APPLICATION NUMBER: PCT/JP97/03711

EARLIER FILING DATE: 1997-10-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence

RESULT 4
Sequence 8, Application US/07876883
Patient No. 5449752

GENERAL INFORMATION:
APPLICANT: Fuji, No. 5449752utaka

APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi

TITLE OF INVENTION: Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883

FILING DATE: 1992-04-29
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.

REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids

TYPE: AMINO ACID
STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-07-876-883-8

Query Match Best Local Similarity 100.0%; Pred. No. 1e-08; Length 19; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMWYRKCKYKGYCYRKCR 18

Db 1 RRWCYRKCYKGYCYRKCR 18

RESULT 5

US-08-426-550-8
 Sequence 8, Application US/08426550
 Patent No. 5710128
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5710128utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsumoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: Pharmaceutical Compositions of Lipopolysaccharide-Binding Polypeptides
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/876,883
 FILING DATE: 19920429
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-07-876-881-20

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-426-550-8

Query Match 100.0%; Score 121; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCVCKCYKGYCVRKCR 18
 Db 1 RRWCYRKCYRGYCVRKCR 18

RESULT 6
 US-07-876-883-20
 Sequence 20, Application US/07876883
 Patent No. 5449752
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5449752utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsumoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: Pharmaceutical Compositions of Lipopolysaccharide-Binding Polypeptides
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/426,550
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids

TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
; US-08-426-550-20

Query Match 97.5%; Score 118; DB 1; Length 18;
; Best Local Similarity 94.4%; Pred. No. 2.4e-08;
; Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRWCYRKCYKGFCYRKCR 18
Db 1 RRWCYRKCYKGFCYRKCR 18

RESULT 8
US-07-876-883-19
; Sequence 19; Application US/07876883
; Patent No. 5449752

GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 115 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550
FILING DATE: 21-APR-1995
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-426-550-19

Query Match 96.7%; Score 117; DB 1; Length 18;
; Best Local Similarity 94.4%; Pred. No. 3.2e-08;
; Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRWCYRKCYKGFCYRKCR 18
Db 1 RRWCYRKCYKGFCYRKCR 18

RESULT 10
US-07-876-883-32
; Sequence 32; Application US/07876883
; Patent No. 5449752

GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 115 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/876,883
 FILING DATE: 19920429
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: peptide
 ; US-07-876-883-32

RESULT 11
 US-08-426-550-32
 Sequence 32, Application US/08426550
 ; Patent No. 5710128
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5710128utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsunoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: Pharmaceutical Compositions of Lipopolysaccharide-Binding Polypeptides
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penile & Edmonds
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/876,883
 FILING DATE: 19920429
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLogy: unknown
 MOLECULE TYPE: peptide
 ; US-07-876-883-15

Query Match 95.0%; Score 115; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.5e-08;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RRWCYRKCKGKCYRKCR 18
 Db 1 RRWCYRKCKGKCYRKCR 18

RESULT 12
 US-07-876-883-15
 Sequence 15, Application US/07876883
 ; Patent No. 5449752
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5449752utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsunoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To Lipopolysaccharides And Their Uses
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penile & Edmonds
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/876,883
 FILING DATE: 19920429
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLogy: unknown
 MOLECULE TYPE: peptide
 ; US-07-876-883-15

Query Match 95.0%; Score 115; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.5e-08;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RRWCYRKCKGKCYRKCR 18
 Db 1 RRWCYRKCKGKCYRKCR 18

RESULT 13
 US-07-876-883-31
 Sequence 31, Application US/07876883
 ; Patent No. 5449752
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5449752utaka
 APPLICANT: Yamamoto, Naoki

APPLICANT: Matsumoto, Akiyoshi
 ATTORNEY: Waki, Michinori
 TITLE OF INVENTION: No. 54,975e1 Polypeptides With Affinity To
 TITLE OF INVENTION: Lipopolysaccharides And Their Uses
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/876, 883
 FILING DATE: 1992-04-29
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 CURRENT APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: 7568-003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 15:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 US-08-426-550-15
 Query Match 95.0%; Score 115; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.5e-08; Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCWCKRKCYKGYCVRKCR 18
 Db 1 RRWCYRKCYKGYCYRKCR 18
 RESULT 14
 US-08-426-550-15
 Sequence 31, Application US/08426550
 Patient No. 5710128
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5710128utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsumoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: Pharmaceutical Compositions of
 TITLE OF INVENTION: No. 5710128e1 Lipopolysaccharide-Binding Polypeptides
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/426, 550
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 31:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-426-550-31

Query Match 95.0%; Score 115; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.5e-08; Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCWCKRKCYKGYCVRKCR 18
 Db 1 RRWCYRKCYKGYCYRKCR 18

RESULT 15
 US-08-426-550-31
 Sequence 31, Application US/08426550
 Patient No. 5710128
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5710128utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsumoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: Pharmaceutical Compositions of
 TITLE OF INVENTION: No. 5710128e1 Lipopolysaccharide-Binding Polypeptides
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/426, 550
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 31:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-426-550-31

Query Match 95.0%; Score 115; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.5e-08; Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCWCKRKCYKGYCVRKCR 18
 Db 1 RRWCYRKCYKGYCYRKCR 18

RESULT 14
 US-08-426-550-15
 Sequence 31, Application US/08426550
 Patient No. 5710128
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5710128utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsumoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: Pharmaceutical Compositions of
 TITLE OF INVENTION: No. 5710128e1 Lipopolysaccharide-Binding Polypeptides
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/426, 550
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 31:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-426-550-31

Query Match 95.0%; Score 115; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.5e-08; Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCWCKRKCYKGYCVRKCR 18
 Db 1 RRWCYRKCYKGYCYRKCR 18

RESULT 15
 US-08-426-550-31
 Sequence 31, Application US/08426550
 Patient No. 5710128
 GENERAL INFORMATION:
 APPLICANT: Fujii, No. 5710128utaka
 APPLICANT: Yamamoto, Naoki
 APPLICANT: Matsumoto, Akiyoshi
 APPLICANT: Waki, Michinori
 TITLE OF INVENTION: Pharmaceutical Compositions of
 TITLE OF INVENTION: No. 5710128e1 Lipopolysaccharide-Binding Polypeptides
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/426, 550
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Miller, Charles E.
 REGISTRATION NUMBER: 24,576
 REFERENCE/DOCKET NUMBER: 7568-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 31:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-426-550-31

Query Match 95.0%; Score 115; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.5e-08; Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRCWCKRKCYKGYCVRKCR 18
 Db 1 RRWCYRKCYKGYCYRKCR 18

Tue May 10 14:34:41 2005

us-10-706-265-2.ral

Page 7

Query Match 95.0%; Score 115; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.5e-08;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRWCYRKCYRKGYCIRKCR 18
Db |||||:|||||:|||:
1 RRWCYRKCYRKGYCIRKCR 18

Search completed: May 9, 2005, 21:15:59
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 9, 2005, 21:08:50 ; Search time 133 Seconds
 (without alignments)
 45.149 Million cell updates/sec

US-10-706-265-2

Title: perfect score: 121 Sequence: 1 RRWCYRKCYKGYCYRKCR 18
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 Sequence: 3 US-09-912-609-117
 Sequence: 4 US-09-917-340-6
 Sequence: 5 US-10-277-232-229
 Sequence: 6 US-10-844-837-6
 Sequence: 7 US-10-838-289-753
 Sequence: 8 US-10-909-119-21
 Sequence: 9 US-10-657-851-6
 Sequence: 10 US-10-042-872-11
 Sequence: 11 US-10-042-872-19
 Sequence: 12 US-10-042-872-4
 Sequence: 13 US-09-030-619-228
 Sequence: 14 US-09-912-609-116
 Sequence: 15 US-09-917-340-5
 Sequence: 16 US-10-042-872-12
 Sequence: 17 US-10-042-872-15
 Sequence: 18 US-10-277-232-228
 Sequence: 19 US-10-042-872-3
 Sequence: 20 US-10-844-837-5
 Sequence: 21 US-10-838-289-752
 Sequence: 22 US-10-909-119-20
 Sequence: 23 US-10-657-851-5
 Sequence: 24 US-10-042-872-3
 Sequence: 25 US-10-042-872-4

Searched: 1428581 seqs, 33359853 residues
 Total number of hits satisfying chosen parameters: 1428581
 Maximum DB seq length: 0
 Minimum DB seq length: 0
 Maximum Match: 100%
 Listing first 45 summaries

Database : Published Applications AA.*
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

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 2: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep: *
 3: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep: *
 4: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep: *
 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep: *
 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
 8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep: *
 9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep: *
 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep: *
 11: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
 12: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *
 13: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep: *
 14: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep: *
 15: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep: *
 16: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep: *
 17: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep: *
 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	121	100.0	18	Sequence 2, Appli
2	106	87.6	18	Sequence 1, Appli
3	106	87.6	18	Sequence 2, Appli
4	106	87.6	18	Sequence 1, Appli
5	106	87.6	18	Sequence 2, Appli
6	106	87.6	18	Sequence 2, Appli
7	103	85.1	18	Sequence 2, Appli
8	103	85.1	18	Sequence 2, Appli
9	103	85.1	18	Sequence 2, Appli
10	103	85.1	18	Sequence 2, Appli
11	103	85.1	18	Sequence 2, Appli
12	103	85.1	18	Sequence 2, Appli
13	96	79.3	18	Sequence 2, Appli

Qry	1	RRWCYRKCYKGYCYRKCR 18
DB	1	RRWCYRKCYKGYCYRKCR 18

RESULT	1	US-10-706-265-2
;	Sequence 2, Application US/10706265	
;	Publication No. US20040132642A1	
;	GENERAL INFORMATION:	
;	APPLICANT: Hwang, Sam	
;	TITLE OF INVENTION: METHODS OF INHIBITING METASTASIS OR GROWTH OF A TUMOR CELL	
;	FILE REFERENCE: 22438	
;	CURRENT APPLICATION NUMBER: US/10/706,265	
;	CURRENT FILING DATE: 2003-11-12	
;	PRIOR APPLICATION NUMBER: 60/425,472	
;	PRIOR FILING DATE: 2002-11-12	
;	PRIOR APPLICATION NUMBER: 60/511,581	
;	NUMBER OF SEQ ID NOS: 11	
;	SOFTWARE: PatentIn version 3.2	
;	SEQ ID NO: 2	
;	LENGTH: 18	
;	TYPE: PRT	
;	FEATURE: Artificial	
;	ORGANISM: Artificial	
;	OTHER INFORMATION: Synthetic	
;	US-10-706-265-2	

Patent No. US20020035061A1
GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; TITLE OF INVENTION: WITH ANTIBIOTICS
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Limulus polyphemus
; US-09-030-619-220

Query Match 87.6%; Score 106; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1;

Qy	Db
1 RRCWYRKCYKGYCYSRKR 18	1 RRWCFRVCKGFCYRKCR 18

RESULT 3
US-09-912-609-108
; Sequence 108, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001-24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-912-609-108

Query Match 87.6%; Score 106; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1;

Qy	Db
1 RRWCYRKCYKGYCYSRKR 18	1 RRWCFRVCKGFCYRKCR 18

RESULT 4
US-10-277-232-220
; Sequence 220, Application US/10277232
; Publication No. US20030221153A1
; GENERAL INFORMATION:

Query Match 87.6%; Score 106; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1;

Qy	Db
1 RRWCYRKCYKGYCYSRKR 18	1 RRWCFRVCKGFCYRKCR 18

RESULT 5
US-10-277-233-220
; Sequence 230, Application US/10277233
; Publication No. US20030232750A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 66081-406C1
; CURRENT APPLICATION NUMBER: US/10/277,233
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Limulus polyphemus
; US-10-277-233-220

Query Match 87.6%; Score 106; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1;

Qy	Db
1 RRWCYRKCYKGYCYSRKR 18	1 RRWCFRVCKGFCYRKCR 18

RESULT 6
US-10-838-289-744
; Sequence 744, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040

CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIORITY APPLICATION NUMBER: US 60/502,429
; PRIORITY FILING DATE: 2003-09-12
; PRIORITY APPLICATION NUMBER: US 60/467,389
; PRIORITY FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 744
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Tumor targeting peptide
; US-10-838-289-744
; Query Match Score 106; DB 17; Length 18;
; Best Local Similarity 87.6%; Pred. No. 1.2e-06;
; Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; Qy 1 RRCWYRKCYKGYCYRKCR 18
; Db 1 RRWCFRVCKGFCYRKCR 18

RESULT 7
US-09-030-619-219
; Sequence 219, Application US/09030619B
; Patent No. US2002003061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081-406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 219
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Limulus polyphemus
; US-09-030-619-219

Query Match Score 103; DB 9; Length 18;
Best Local Similarity 77.3%; Pred. No. 1.2e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
; Qy 1 RRCWYRKCYKGYCYRKCR 18
; Db 1 RRWCFRVCKGFCYRKCR 18

RESULT 8
US-09-912-609-107
; Sequence 219, Application US/09030619B
; Publication No. US2002003061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081-406C1
; CURRENT APPLICATION NUMBER: US/10/912,609
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 232

RESULT 9
US-10-042-872-13
; Sequence 13, Application US/10042872
; Publication No. US2002015601A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Zhang, Lijuan
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF
; FILE REFERENCE: UBC1170-1
; CURRENT APPLICATION NUMBER: US/10/042,872
; CURRENT FILING DATE: 2002-01-08
; PRIORITY APPLICATION NUMBER: US 09/604,864
; PRIORITY FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Limulus polyphemus
; US-10-042-872-13

Query Match Score 103; DB 13; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
; Qy 1 RRCWYRKCYKGYCYRKCR 18
; Db 1 RRWCFRVCKGFCYRKCR 18

RESULT 10
US-10-277-232-219
; Sequence 219, Application US/10277232
; Publication No. US20030211537A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081-406C1
; CURRENT APPLICATION NUMBER: US/10/277,232
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 232

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 219

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Limulus polyphemus

; US-10-277-233-219

Query Match 85.1%; Score 103; DB 15; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRMWCYRKCYKGYCYRKCR 18
Db 1 RRMCFRVCYRGFCYRKCR 18

RESULT 11

US-10-277-233-219

; Sequence 219, Application US/10277233

; Publication No. US20030232750A1

; GENERAL INFORMATION:

; APPLICANT: Krieger, Timothy J.

; APPLICANT: Taylor, Robert

; APPLICANT: Erfile, Douglas

; APPLICANT: Fraser, Janet R.

; APPLICANT: West, Michael H.P.

; APPLICANT: McNicol, Patricia J.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

; TITLE OF INVENTION: WITH ANTIBIOTICS

; FILE REFERENCE: 660081-406C1

; CURRENT APPLICATION NUMBER: US/10/277,233

; CURRENT FILING DATE: 2005-10-18

; NUMBER OF SEQ ID NOS: 232

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 219

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Limulus polyphemus

; US-10-277-233-219

Query Match Best Local Similarity 85.1%; Score 103; DB 15; Length 18;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRMWCYRKCYKGYCYRKCR 18
Db 1 RRMCFRVCYRGFCYRKCR 18

; OTHER INFORMATION: Tumor targeting peptide
; US-10-838-289-743

; Query Match 85.1%; Score 103; DB 17; Length 18;

; Best Local Similarity 77.8%; Pred. No. 2.9e-06; Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRMWCYRKCYKGYCYRKCR 18
Db 1 RRMCFRVCYRGFCYRKCR 18

RESULT 13

US-10-042-872-18

; Sequence 18, Application US/10042872

; Publication No. US20020156017A1

; GENERAL INFORMATION:

; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA

; APPLICANT: Hancock, Robert E. W.

; APPLICANT: Zhang, LiJuan

; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF

; TITLE OF INVENTION: USE THEREOF

; FILE REFERENCE: UBC1170-1

; CURRENT APPLICATION NUMBER: US/10/042,872

; PRIOR APPLICATION NUMBER: US 09/604,864

; CURRENT FILING DATE: 2002-01-08

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: cationic antimicrobial peptide

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 5

; OTHER INFORMATION: Xaa is an amino acid having a basic side chain

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 10

; OTHER INFORMATION: Xaa is an amino acid having an aromatic side chain or an aliphatic

; US-10-042-872-18

; Sequence 10, Application US/10042872

; Publication No. US20020156017A1

; GENERAL INFORMATION:

; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA

; APPLICANT: Hancock, Robert E. W.

; APPLICANT: Zhang, LiJuan

; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF

; TITLE OF INVENTION: USE THEREOF

; FILE REFERENCE: UBC1170-1

; CURRENT APPLICATION NUMBER: US/10/042,872

; CURRENT FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 09/604,864

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSEQ for Windows Version 4.0

; LENGTH: 18

; GENERAL INFORMATION:
; APPLICANT: Gao, Jiming
; Sequence 743, Application US/10838289
; Publication No. US20050058603A1
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHells
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 743
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

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; TYPE: PRT
; ORGANISM: Limulus polyphemus
US-10-042-872-10

Query Match          78.5%; Score 95; DB 13; Length 18;
Best Local Similarity    77.8%; Pred. No. 2.9e-05;
Matches   14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy      1 RRWCYRKCYKGCYRKCR 18
        ||||| | :||||| |
Db      1 RRWCYRKCYAGCYRKCR 18

RESULT 15
US-09-030-619-229
; Sequence 229, Application US/09030619B
; Patent No. US20020035061A1

GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Faber, Janet R.
; APPLICANT: West, Michael R.P.
; APPLICANT: Menicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081..06

CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 229
LENGTH: 17
TYPE: PRT
ORGANISM: Tachyporus tridentatus
US-09-030-619-229

Query Match          77.7%; Score 94; DB 9; Length 17;
Best Local Similarity    76.5%; Pred. No. 3.6e-05;
Matches   13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy      2 RWCCYRKCYKGCKCR 18
        ||||| | :||||| |
Db      1 RWCFRVCYRGICYRKCR 17

Search completed: May 9, 2005, 21:18:18
Job time : 134 secs

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